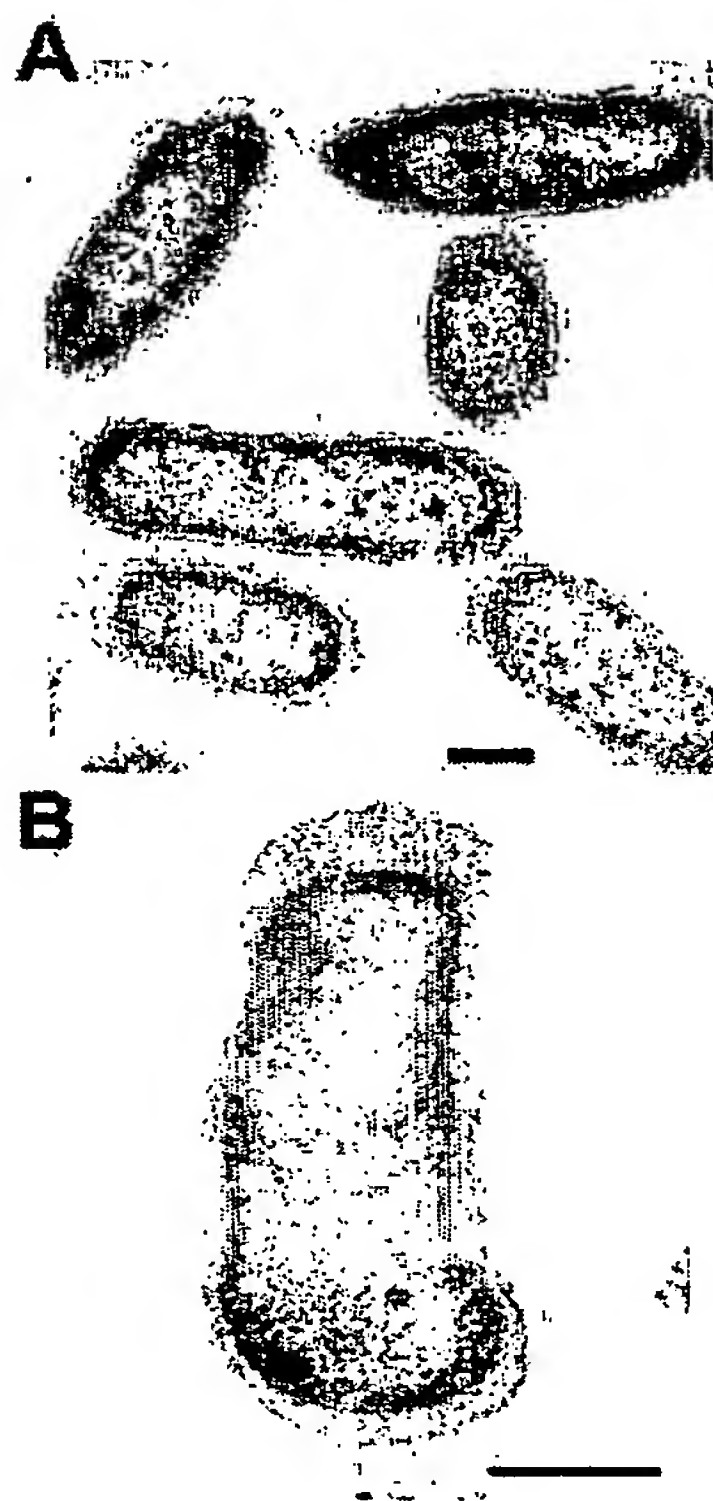


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FIGURES

FIG. 1



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FIG. 2

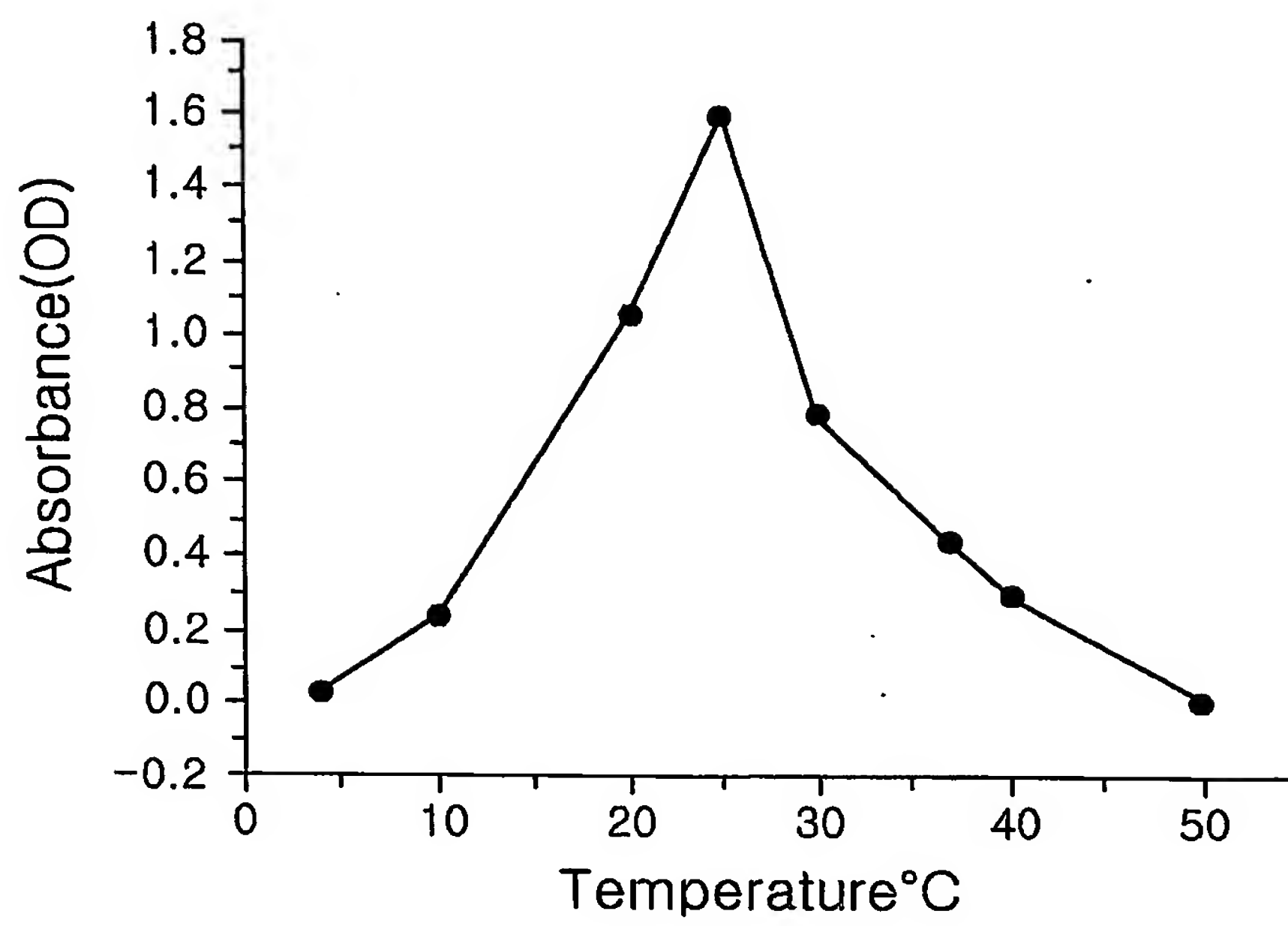
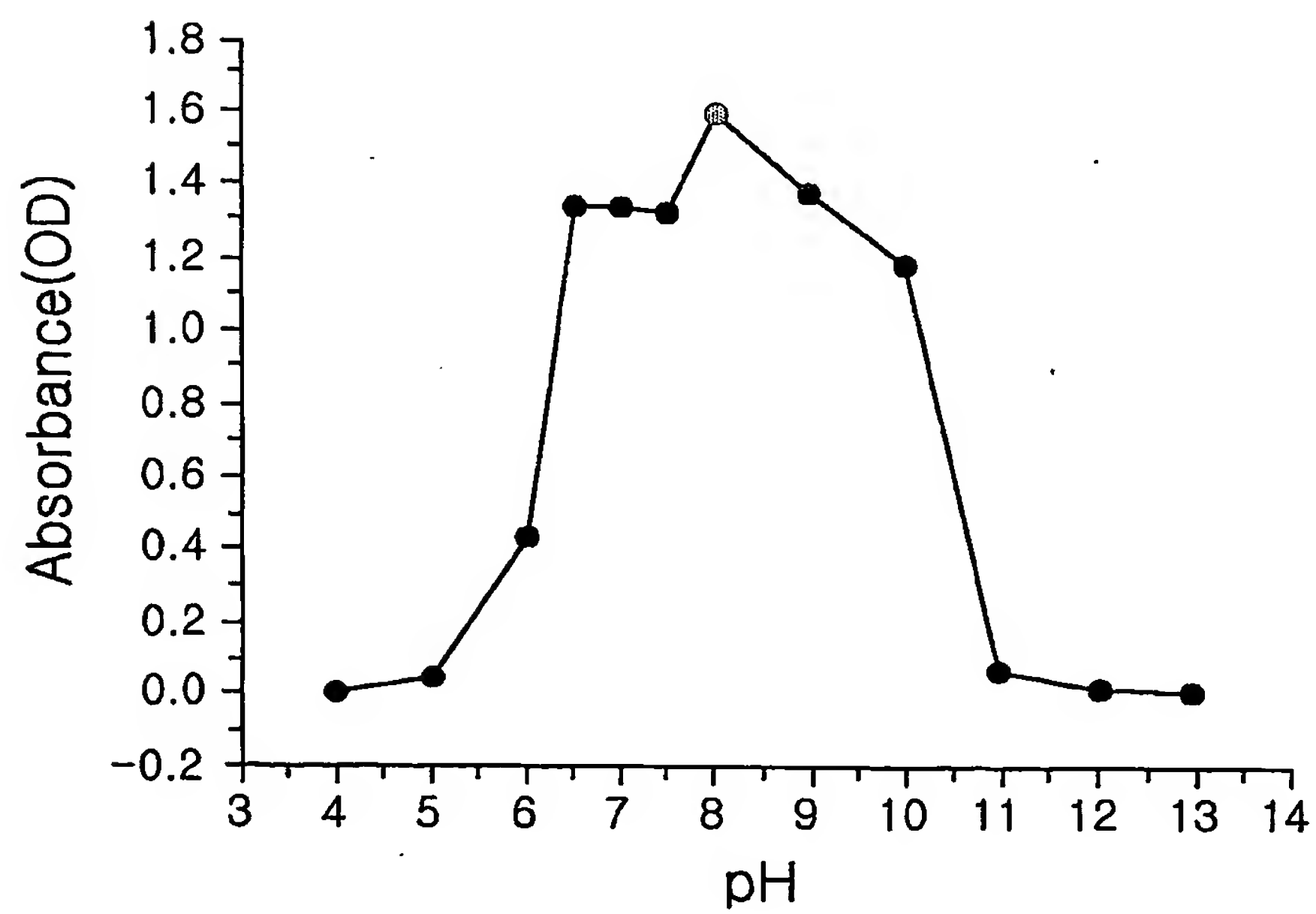


FIG. 3



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FIG. 4

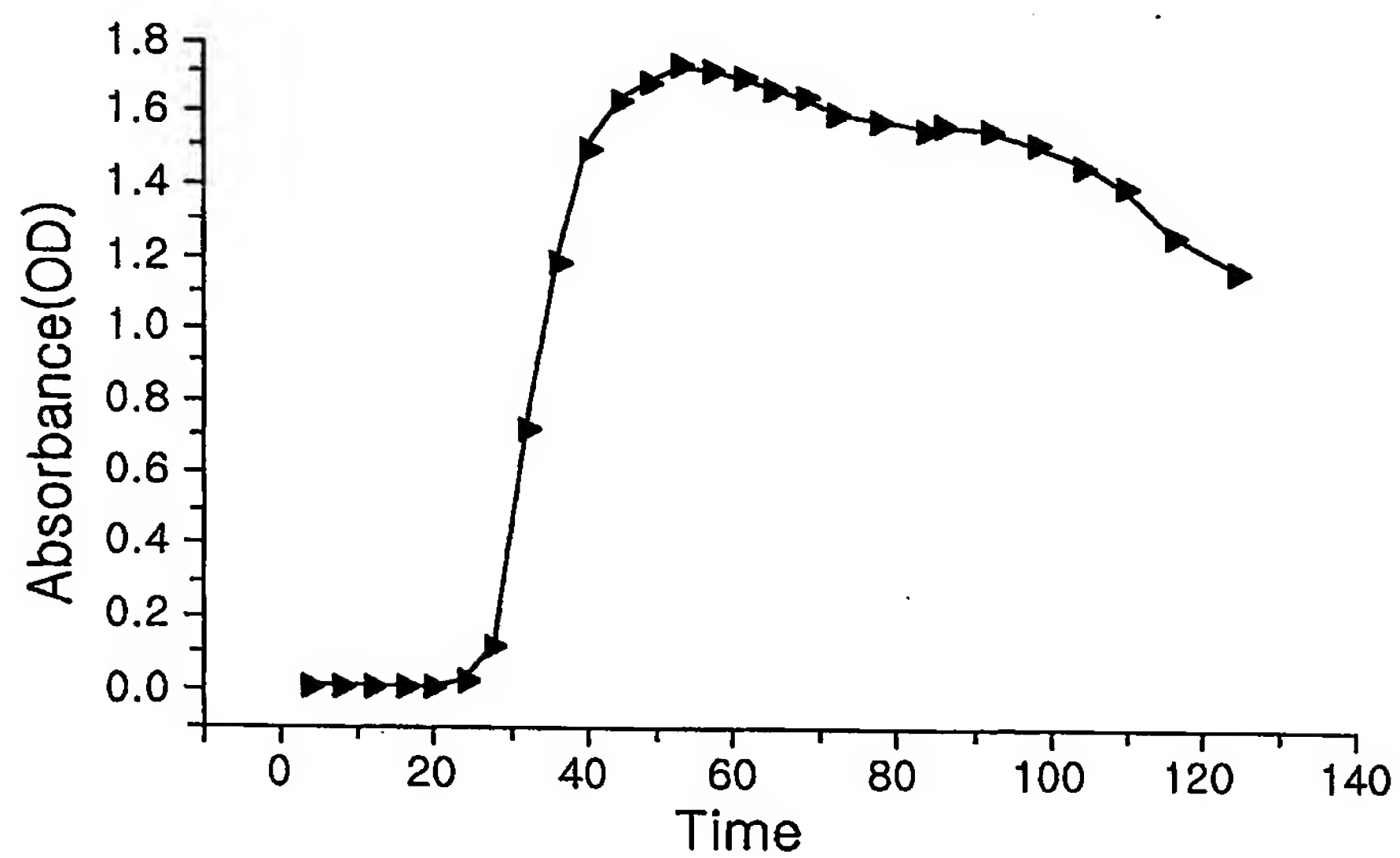
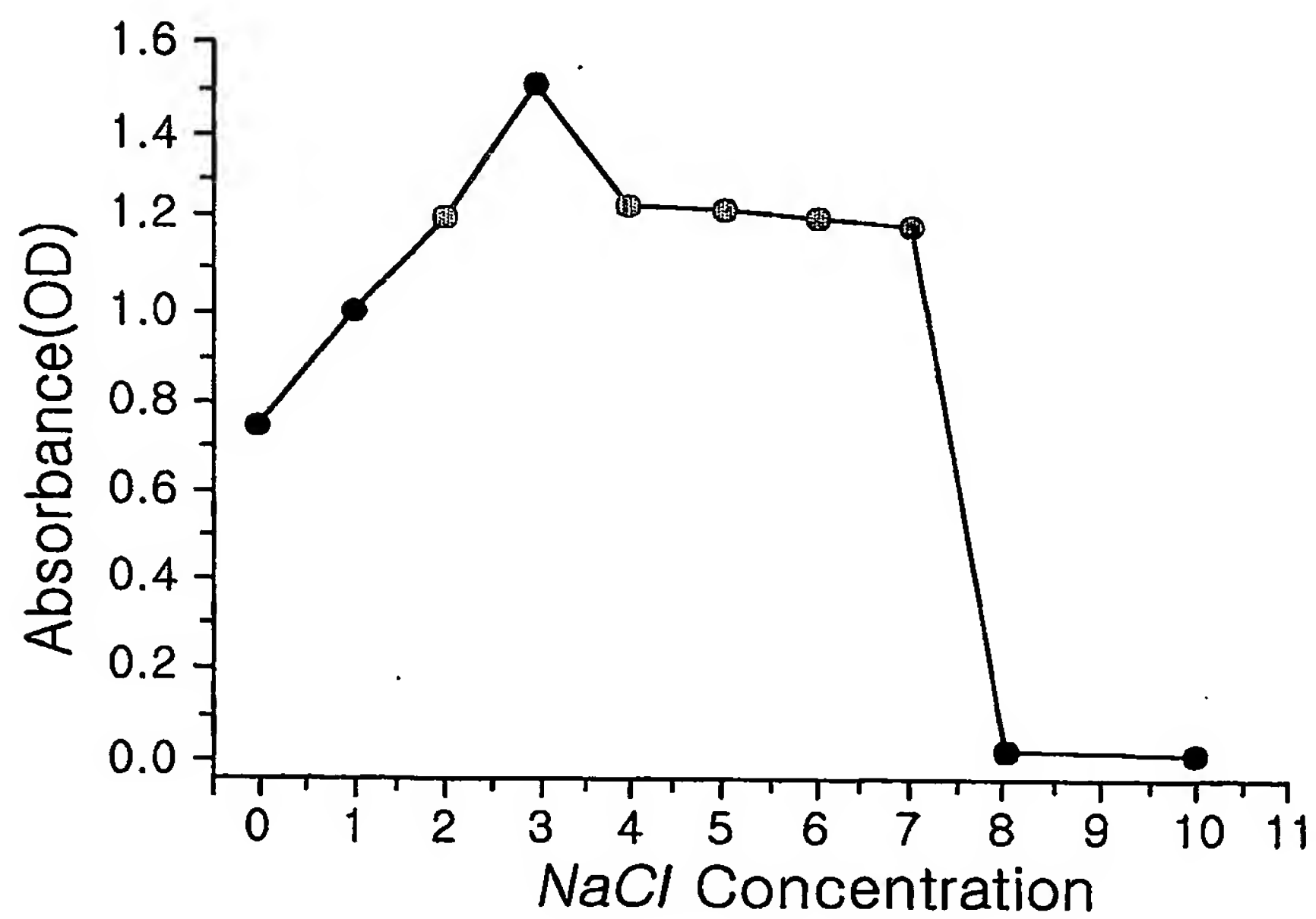
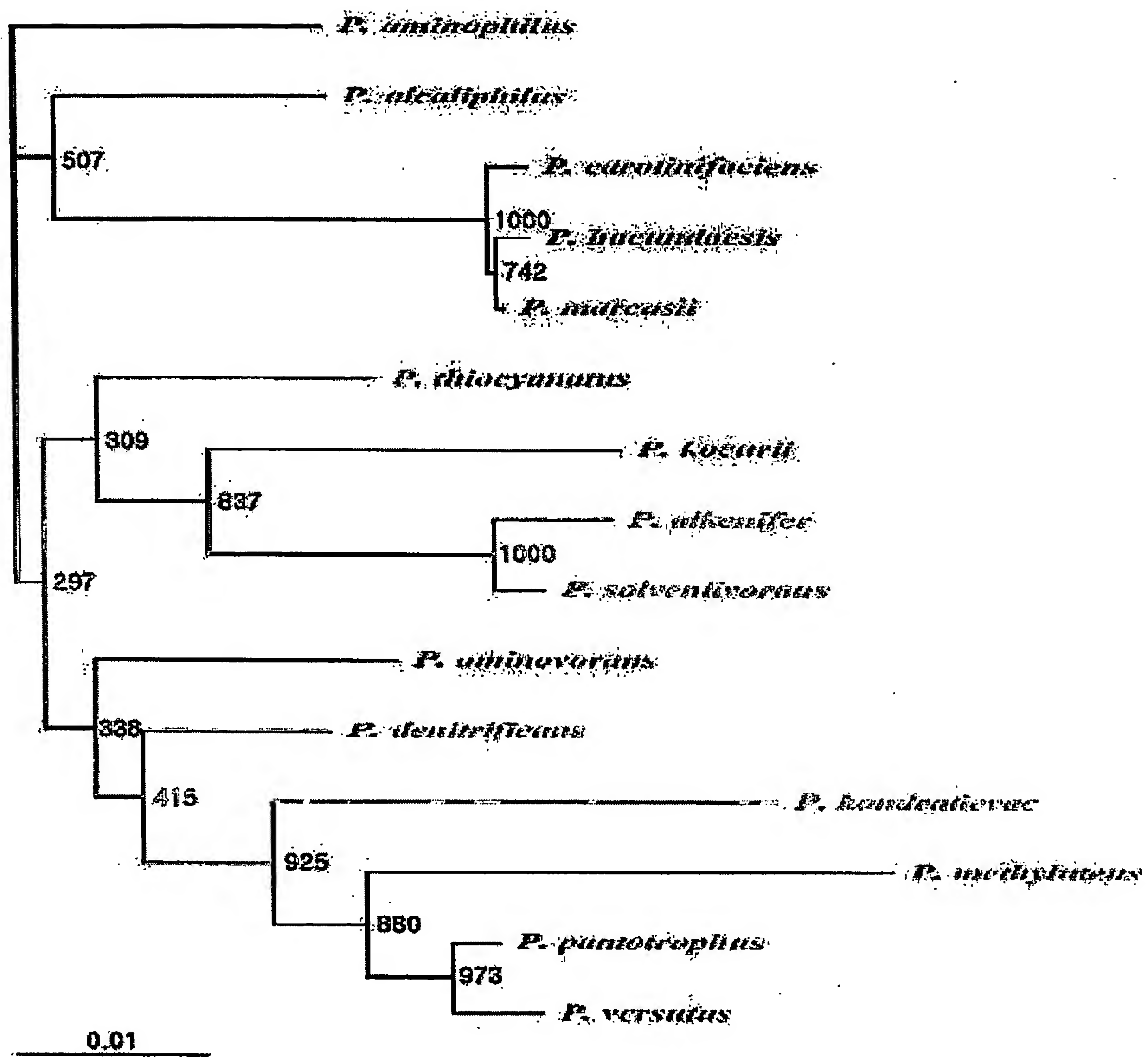


FIG. 5



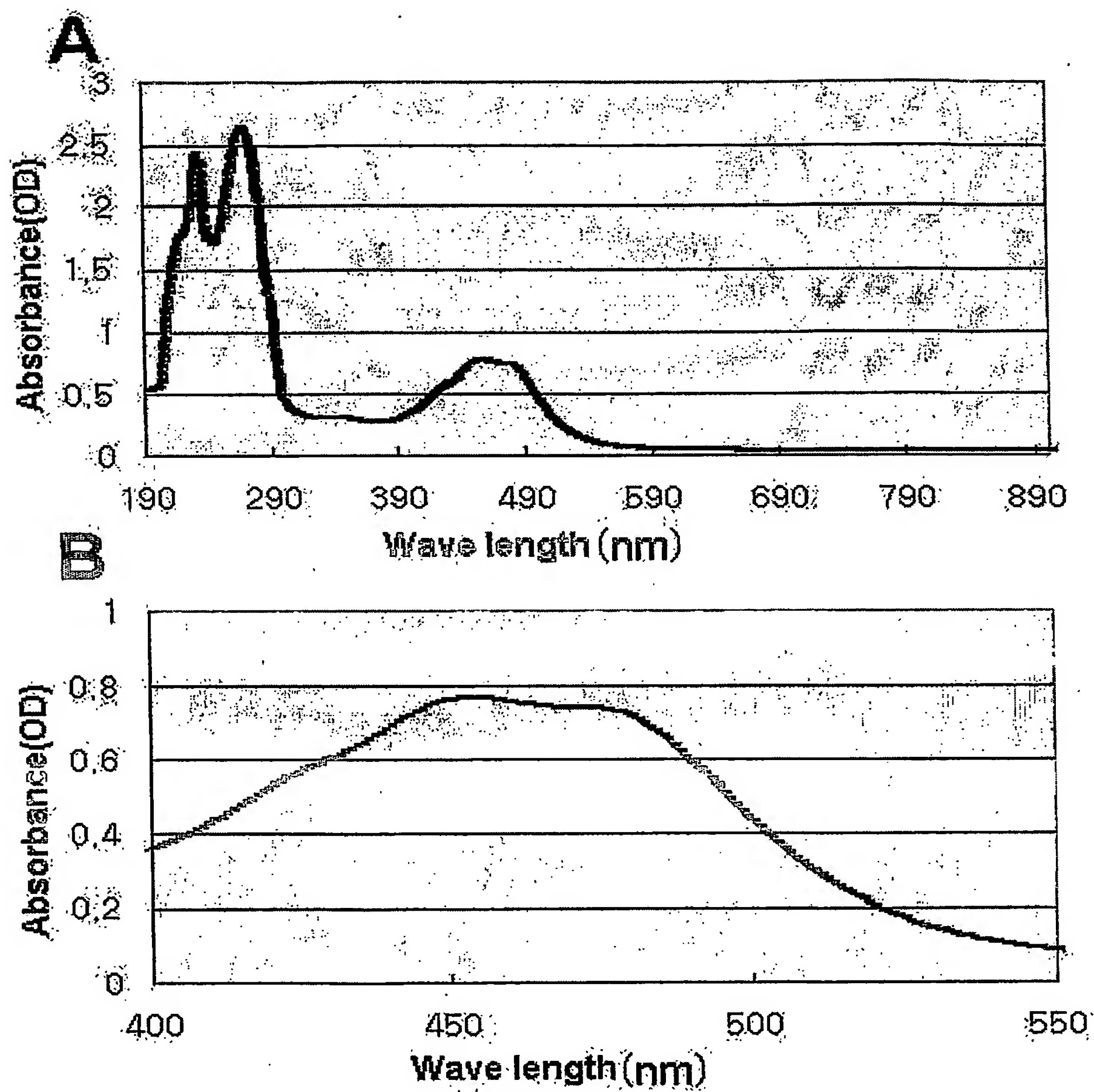
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FIG. 6



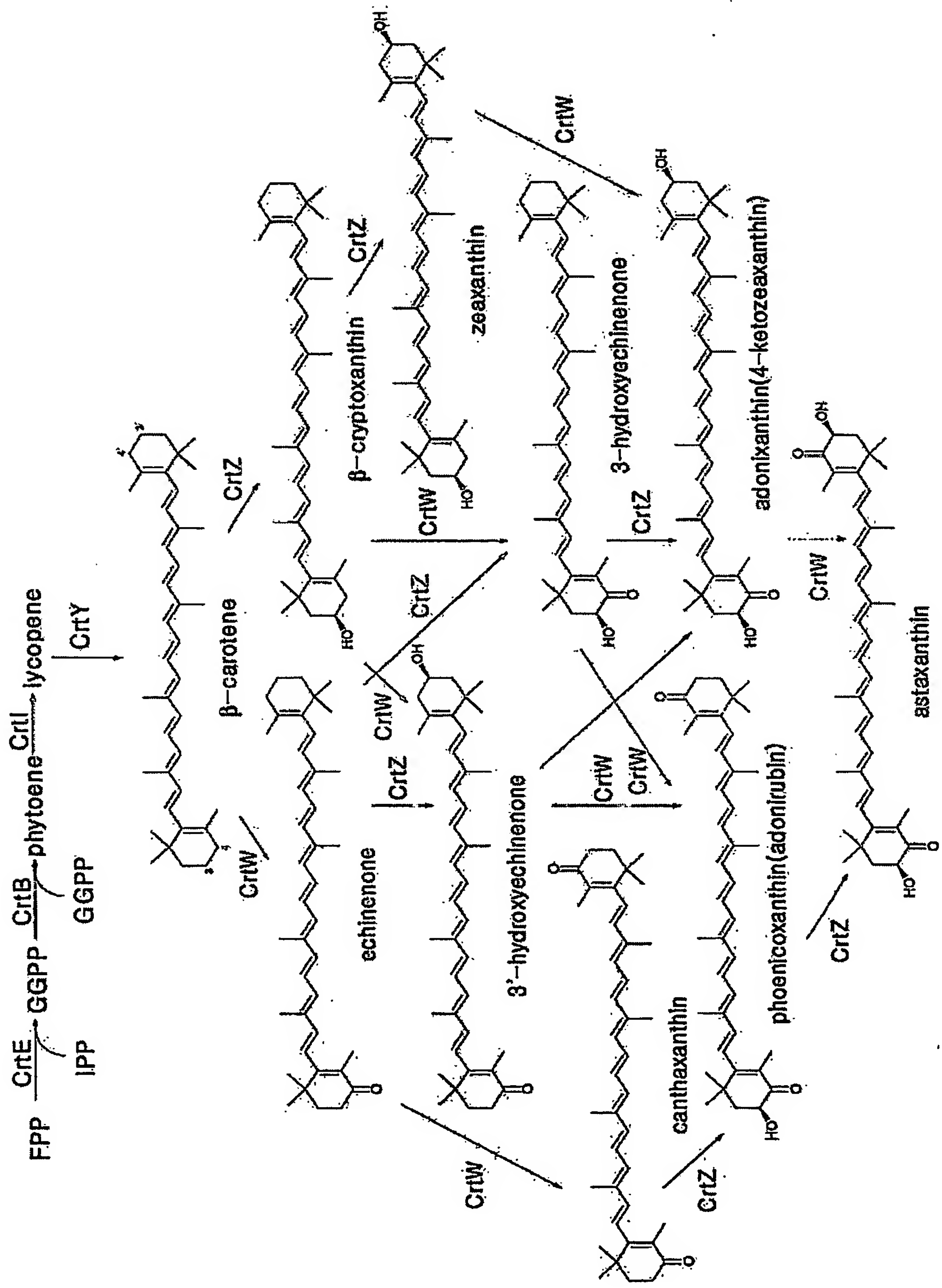
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FIG. 7



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FIG. 8



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FIG. 9

	1		100
P. haendaesis	(1)	MSAHALPKADLTATSLIYSGGIIAANLALHVBALWFLDAAAHPI LAIANELQLT-WLSVGLPFI AHDAHHSVYVGRPRGNAANGQLVLE	
Alcaligenes_sp	(1)	MSGRKPGTIGDTIVMLGLTAAI LLCLVLHAFILWLLDAAAHPLCAVLCAGLT-WLSVGLPFI AHDAHHSVYVGRPRBANAAGQLALQ	
Bradyrhizobium_sp	(1)	MHAATAKATEFGASRRDDARORRVGLTAAVITAAWLVHVGLENFEWPLTLHSLPALPLVVLQWLYVGLFI AHDCHEGSLVPEKPKQVHRIQQLCLF	
Consensus	(1)	MSA K A T V L LSAALIAAQLVLEWFLDAAAHPLLA L LGLT WLSVGLPFI AHDAHHSVYVGRPRBANAAGQL LV	
	101		200
P. haendaesis	(90)	LYAGFSWRKNIYKHNAHHRBTGDDDDPFDHG--GPVRYARFIGTYEGWREGLLPVI VT VYALILGD-RWYVVFQPLPSTLSTQLFVFGTULPHR	
Alcaligenes_sp	(90)	LYAGFSWPKLIAKHNT HHRHAGTDNDPFDHG--GPVRYQSRVSTYEGWREGLLPVI VT VYALILGD-RWYVVFQPLPSTLSTQLFVFGTULPHR	
Bradyrhizobium_sp	(101)	LYAGFSFDALNVHHRHHRHBTGAELEDEVPFGFQWFFASFELEHFGKQVAIAAVSLVYQLVFAVPLQNILFSAEPGLLSAQGLT FGTVEFRR	
Consensus	(101)	LYAGFSW KLIVKHM HHRH GTDDDPFDHG GPVRYASFI TYEGWREGLLPVI VT VYALILGD RWYVVFQPLPAI LSTQLFVFGTULPHR	
	201		289
P. haendaesis	(186)	PGHDAFPDRBNARSSRISDPVSLTCTFHGGYHSHHLEPTVFWRLPSTRTKGDTA--	
Alcaligenes_sp	(186)	PGHDDFPDRBNARSTGIGDPLSLTCTFHGGYHSHHLEPTVFWRLPSTRTKIGRA--	
Bradyrhizobium_sp	(201)	PATQFPADRNARSTSEPPAWLSLLTCTFHGGYHSHHLEPTVFWRLPSTRTKRALEERD	
Consensus	(201)	PGHD FPDNRNARSS I DPLSLTCTFHGGYHSHHLEPTVFWRLP T RKG A	

FIG. 10

	1		100
P. haendaesis	(1)	HTNELIVVATVLVHETAYSVHRWIMHGPFGGQHKSHHEERHDALEKNDLYGLVFAVIATVLFVQWIGAPVLWVIALGHTVYGLIYFVLHDLVQRQ	
Alcaligenes_sp	(1)	HTNELIVVATVLVHETAYSVHRWIMHGPFGGQHKSHHEERHDALEKNDLYGLVFAVIATVLFVQWIGAPVLWVIALGHTVYGLIYFVLHDLVQRQ	
Consensus	(1)	HTNELIVVATVLVHETAYSVHRWIMHGPFGGQHKSHHEERHDALEKNDLYGLVFAVIATVLFVQWIGAPVLWVIALGHTVYGLIYFVLHDLVQRQ	
	101		163
P. haendaesis	(101)	PFRYIPRKYARLYQAHLHHAVEGRDHCVSFGFIYAPPVQKLKQDLKSGVLEBAQERT	
Alcaligenes_sp	(101)	PFRYIPRKYARLYQAHLHHAVEGRDHCVSFGFIYAPPVQKLKQDLKSGVLEBAQERT	
Consensus	(101)	PFRYIPRKY BRLYQAHLHHAVEGRDHCVSFGFIYAPPVQKLKQDLK SGVLE S	

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FIG. 11

	1	100
<i>P. haemundae</i>	(1) VTHVLLAGAGLANGLIALALBAARDLEVLDDHAAGPSQGHVSCDPPDLSPHOLARLEKPIRANWPDQEVFPFHARBLATGVCSLDGAALADAVAR	
<i>Flavobacterium_sp</i>	(1) NSHDLIAGAGLSGALIALAVEDREDAI VMLDARSQPSIQHTQCCHUTDLSPFWLADLSPIRESEHTDQEVAFPDSERLITGVQSIHAGALIGLLQ-	
Consensus	(1) NSHDLIAGAGLA ALIALALB RPD RILLDD AGPSD HTSCHD DLSP WLARL PIRRA Q DQEV FP HARBL TGVCSIDAAAL L	
	101	200
<i>P. haemundae</i>	(101) SGARISWSDIALLDQCATLSGTEIRAGAVLDGRGAQPSRHITVGFQRFYGVRIETDCPHGVPPHENDATVITQDQYEFITLLPSPTRILIEDTRY	
<i>Flavobacterium_sp</i>	(100) -GVDLRHTHTVATLDGTATLTDGSEIRAACTIDALQAVETPRLTVIPQKFTYGVRIETDAPHGVPPHENDATVITQDQYEFITLLPSPTRILIEDTRY	
Consensus	(101) G DIRVNS IA LDD GATLS GSRIRAA VIDARGA S HLTVGQRFYGVRIETD PHGV RPHINDATV Q DQYEFITLLPSPTRILIEDTRY	
	201	300
<i>P. haemundae</i>	(201) SDGQNLDDALAAASHDYARQQGUTGAHVRRERGLPIALABDAAGFWADHAGGVPPVGLBAGFFHPTGTSLYAAQVADVAGLSGPPCTDALRGAR	
<i>Flavobacterium_sp</i>	(199) SDGIDLDDGALAAALDYAARRQUTGQNKSEEGITPIALABDAAGFWADHAGGVPPVGLBAGFFHPTGTSLYAAQVADALAAAR--DLTASARRAVE	
Consensus	(201) SDGG LDD ALA AS DYA GWTG HMRERERGLPIALABDA GFQ DBA G VPVGL AG FHPVTGYSLPYAAQVAD IAA T A R AIR	
	301	387
<i>P. haemundae</i>	(301) DYALDKAREDEFLRLNRLFRGCGAPDRBYTLLQEFYHNPBGLIEPZYAGRLSVADQLRI VTKPPITPLGTATIECLPEEPILKENA	
<i>Flavobacterium_sp</i>	(297) GWALDKAREDEFLRLNRLFRGCGAPDRBYTLLQEFYHNPBGLIEPZYAGRLSVADQLRI VTKPPITPLGTATIECLPEEPILKENA	
Consensus	(301) WADRA RDRFLRLNRLFRGC PDRBY LLQRFYRLP LIRFYAGRLSLAD LRI VTKPPITPL AIRCLPERPLL E A	

FIG. 12

	1	100
<i>P. haemundae</i>	(1) HNAHSPAANTHITIGAGFGALALAIRLQSAAGIATTLYEADDEFGGATFTHDQGHVFDAGETITDPDALKEGLALTOGDHAEVTLHPTVFFYLHUPG	
<i>Flavobacterium_sp</i>	(1) -----HSSATIGAGFGALALAIRLQSAAGIATTIYBARIKFGGATFTHDQGHVFDAGETITDPDALKEGLALTOGDHAEVTLHPTVFFYLHUPG	
Consensus	(1) S TIVIGAGFGALALAIRLQSAAGIATTIYBARDKPGGATFTHDQGHVFDAGETITDPDALKEGLALTOGDHAEVTLHPTVFFYLHUPG	
	101	200
<i>P. haemundae</i>	(101) GKVFDYVNEALQLELQIAQFLDDELYGYSERDYAESYQGGYALQVITFLQLQLEKAPALHKLKAYKE SHAKVATFIRDPYLLKAPSYELLLWQH	
<i>Flavobacterium_sp</i>	(94) GRSFEPVHDDREITQVASEFPADVQYERHDFAEVFRQYELHGTTPFLKQGLNNAFALALRLQATRE VHSHPAREIQDEHLTAAPFETLLVQNH	
Consensus	(101) GK FDYVND D L BQIA FNP DLDGYRRF DYAREVY EGYLRLGT PFLKQGLN NAAPALHKL AYKSVHA VA FI DPHLRQAFSPHTLLVQGN	
	201	300
<i>P. haemundae</i>	(201) PFSTSSIALIHALEREGGVWFAKGGTNQLVAGHVALFERLGGQNNLNAKVAHETEGARTTGVTLADGESLKADEWASNGVHNYHLLGETAGQSR	
<i>Flavobacterium_sp</i>	(194) PFSTSSIALIHALEREGGVWFAKGGTNQLVAGHVALFERLGGQNNLNAKVAHETEGARTTGVTLADGESLKADEWASNGVHNYHLLGETAGQSR	
Consensus	(201) PFSTSSIALIHALEREGGVWFAKGGTNQLVAGHVALFERLGGQNNLNAKVAHETEGARTTGVTLADGESLKADEWASNGVHNYHLLGETAGQSR	
	301	400
<i>P. haemundae</i>	(301) ASSLDEKRVSHVFLHFGLEAPKDIAHNTILFQPEYRRIVHEIFKGFELAEFSLYLSRPTTDPDNAPPGETSYVLAAPVPHLRABIDGAVGPRY	
<i>Flavobacterium_sp</i>	(294) AAILNRQWCHLEFLHFGLEAPKDIAHNTILFQPEYRRIVHEIFKGFELAEFSLYLSRPTTDPDNAPPGETSYVLAAPVPHLRABIDGAVGPRY	
Consensus	(301) A L R RVSHSLFVLFGL P IAHHSIIFGPRYK LVNEIF GPKL DDFSLYLSRPTTDP LAP GMSHYVLAAPVPHLRADIDV EAP Y	
	401	500
<i>P. haemundae</i>	(401) ADKILASLEELIPNLRLNLTITRIPTPADFASLNAHGGAPSVPEPILTQAWFRPHNDKTI RNFYLVGAGTHPGAGIPGVVGS AKAT AQVHLSDLAQ	
<i>Flavobacterium_sp</i>	(394) ABRIFEELERRAIPDLRLHLTVSEIFSPADPSTHLSAHGSAFVPEPILTQAWFRPHNDKTI RNFYLVGAGTHPGAGIPGVVGS AKAT AQVHLSDLAQ	
Consensus	(401) ADRI LE R IP LR LT SRIFSPADFASL AHGSAFVPEPILTQAWFRPHNDK I NFYLVGAGTHPGAGIPGVVGS AKAT AQVHLSDLA	
	501	
<i>P. haemundae</i>	(501) A	

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FIG. 13

	1	100
<i>P. haemdaesis</i>	(1) MSDLVLTSTRAITQSSQSFATAAKLHPFPIRDDTVHLYAVCRHADDVIDGIALGSRPEAVNDPQARLDGLRVDTLAALQGDGPVTFPAALBAYARRHDF	
<i>Flavobacterium_sp</i>	(1) HTDLTATSEAAIAGQSCSFAQAARIMPPGIRBDTVHLYAVCRHADDVIDGQVMSAPRAGGPPQARLGARADTFAALHBDGPHSPFPAALBQVARRHDF	
Consensus	(1) MSDL TS AI QGSQSF AAKLHPPGIRDDTVHLYAVCRHADDVIDGQ LGS PBA DPQARL ALR DTLAAL DGPMSPPFAALB VARRHDF	
	101	200
<i>P. haemdaesis</i>	(101) PQAWFNDLIEGFANDVEARDVETLDDVLEYSTYHAGIVGVNBARVEGVRRDPVLDRAQDLGLAFCLTHIARDVIDDARIIGCYLPQDGLDQAGARIDGPT	
<i>Flavobacterium_sp</i>	(101) EDLWFNDLIEGFANDVADREYSLDDVLEYSTYHAGIVGVNBARVHVQDDAVLDEASDLGLAFQLTNIARDVIDDAAIGCYLPADGLABAGATVEGPT	
Consensus	(101) P WFNDLIEGFANDV EDYBSLDDVLEYSTYHAGIVGVNBARVHVQ DD VLDRAQDLGLAFQLTNIARDVIDDA IGRCYLPADWL AGA IDGPT	
	201	300
<i>P. haemdaesis</i>	(201) ESPELYTVILRLDEAEYYSARYBLADLPPECANSI AALRIYTHAIGLRIKSGPQAVRQRISTSKAAKIGLLGVGGQDVARSLLPGAGVSBQGLNTE	
<i>Flavobacterium_sp</i>	(201) EDALYSVIRLLDAAEPTTASARQGLPHLPPECANSI AALRIYTHAIGLRIKSGPQAVRQRISTSKAAKIGLLABGGLDAAASLLRGGHISBDGLNTE	
Consensus	(201) ES LYSVIRLLD AEPYTSAR GL LPPECANSIAALRIYTHAIG RIR GP AVQRISTSKAAKIGLLA GG D A SBL GA ISB GLNTE	
	301	
<i>P. haemdaesis</i>	(301) PHHV	
<i>Flavobacterium_sp</i>	(301) FRA-	
Consensus	(301) P	

FIG. 14

	1	100
<i>P. haemdaesis</i>	(1) URRDVNPITHATLLQTLLEBIAQGTCAVSQPLQAMVCHGALSSIREFQMLLELLAAEAMGGVCDTIYDAACAVENHVAASLIQDLECYTDAGLSECRPAT	
<i>Flavobacterium_sp</i>	(1) ITPKQPPRLDLVHIRLAQISGQREYSAFLQAAKSDAALSPOKEFRAVLHLVVAESSGQVCDANVDAACAVENHVAASLIQDNIQHDDARTAEHQPAT	
Consensus	(1) N N LL RL IA FG VS PLGAANS AALS GKRFRAHLHL AASGGVCD IVDAACAVENHVAASLIQDLPCHDDA BRG PAT	
	101	200
<i>P. haemdaesis</i>	(101) HVANGESDAVLGGI ALITYAHALLAGAGASGTVTAQLVRILSSSLAQQLCAGQDLHLAAKNGAGVEQDLEKTVLFIAGLEHLAVIEKFDABDQTQ	
<i>Flavobacterium_sp</i>	(101) HVANGEGRAYLAGI ALITYAHIRLGEAGATPDQEARLYASEEAMTEVLCAGQDLHLAPKDAACIEEQDLEKTVLFIAGLEHLAVIEKFDABDQTQ	
Consensus	(101) HVANGS BAVLAGIALITEAM ILA AGAS RA LV LSRALGP GLCAGQDLHLA K AAGIE EQDLEKTVLFIAGLEHLAVIE D B Q	
	201	295
<i>P. haemdaesis</i>	(201) MIDFGQLGRVFCSYDDLLDVYQDQALGKDTGDDAFADEPRRILLAYSDLQNTSBHYEASRAQLI ANLSKRLQAPRI AALLERVLPAALAA--	
<i>Flavobacterium_sp</i>	(201) LNAFGQLGRVFCSYDDLLDVIGDKASTGRDTARDTAPGPGGIMAVGQMGDTAQHYBASBAQLDELHETRLFRGGQIADLLASVLPEDIRSA	
Consensus	(201) LI FGRQLGRVFCSYDDLLDVIGD AA GRDTARD AAPGPK GILLAV L VA HY ASBAQLD LLRSK A IA LL RVLPH R	

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FIG. 15

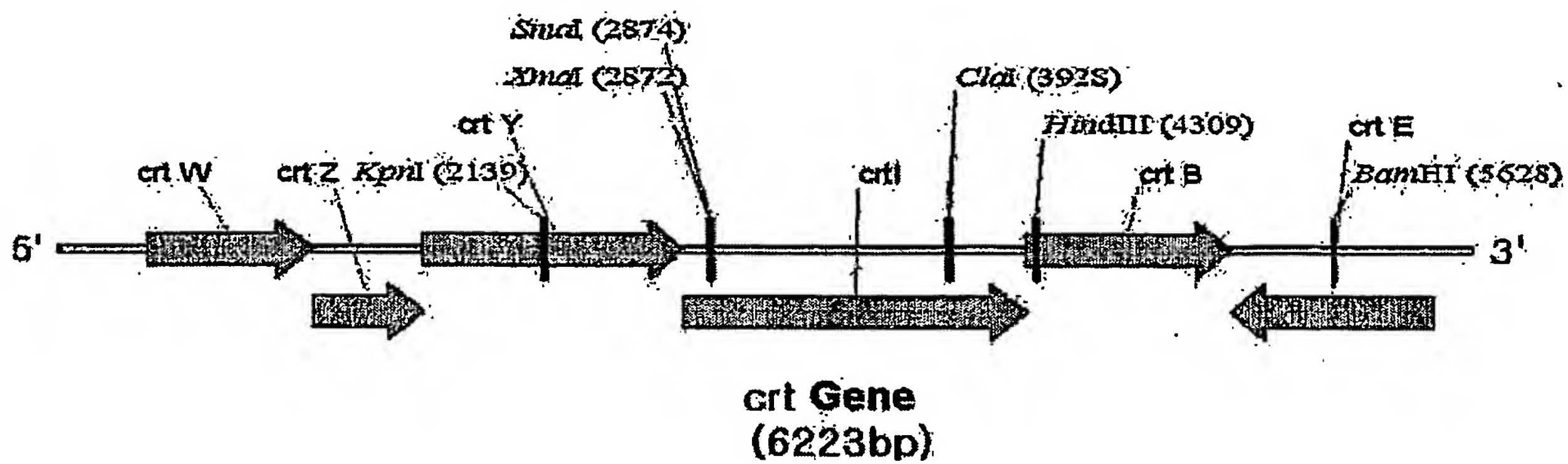
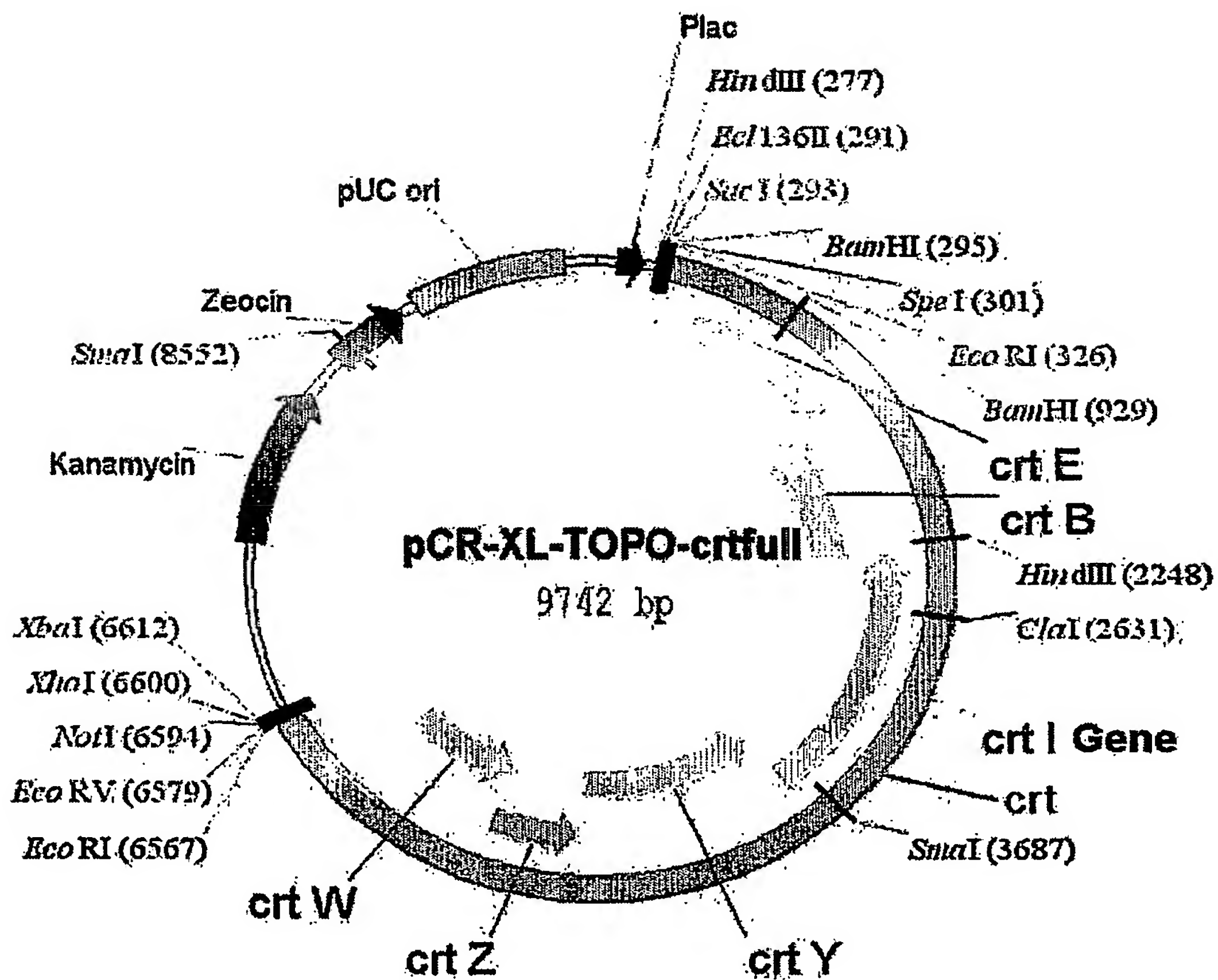


FIG. 16



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FIG. 17

